

TEAM 4

PAGE: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/08/793,408

DATE: 09/25/97 TIME: 12:34:44

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This Raw Listing contains the General Information Section and up to the first 5 pages.

1	,	SEQUENCE LISTING	TERED
2 3	(1) Conor	al Information.	E
4	(1) Gener	al Information:	GRA.
5	(i) APP	LICANT: Choo, Yen	, CV
6		Klug, Aaron	
7		Sanchez Garcia, Isidro	
8 9	/44\ mTm	TE OF INVENTION. Improvements in an helating to	
10		LE OF INVENTION: Improvements in or Relating to ding Proteins for Recognition of DNA	
11	D111	dring frotering for Recognition of DRA	570.
12	(iii) NUM	BER OF SEQUENCES: 18	BECEIVED
13			
14	• •	RESPONDENCE ADDRESS:	NOV 0 4 1997,
15 16) ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.) STREET: 1100 New York Avenue, N.W.	10703
17	·) CITY: Washington	anoup 1800
18	•) STATE: D.C.	C.11001 1000
19	•) COUNTRY: USA	
20	(F) ZIP: 20005-3918	
21			
22 23	• •	PUTER READABLE FORM:	
24) MEDIUM TYPE: Floppy disk) COMPUTER: IBM PC compatible	
25) OPERATING SYSTEM: PC-DOS/MS-DOS	
26	•) SOFTWARE: Word Perfect	
27			
28	• •	RENT APPLICATION DATA:	
29 30	•) APPLICATION NUMBER:	
31	•) FILING DATE:) CLASSIFICATION:	
32	(0	, CDADDILICATION.	•
33	(vii) PRI	OR APPLICATION DATA:	
34	•) APPLICATION NUMBER: PCT/GB95/01949	
35	(B) FILING DATE: 17-AUG-1995	
36 37	(wii) DDT	OR APPLICATION DATA:	
38	, ,) APPLICATION NUMBER: GB 9514698.1	
39	•) FILING DATE: 18-JUL-1995	
40	•		b
41	• •	OR APPLICATION DATA:	-
42	•) APPLICATION NUMBER: GB 9422534.9	
43 44	(В) FILING DATE: 08-NOV-1994	·
45	(vii) PRT	OR APPLICATION DATA:	· · · · · · · · · · · · · · · · · · ·
46	•	OR APPLICATION NUMBER: GB 9422334.9 OR APPLICATION DATA:) APPLICATION NUMBER: GB 9416880.4	• .

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17			(B) FI	LING	DAT	E: 2	0-AU	3-19	94	. 19. a .		•	
18 19	(2)	INFO	RMAT:	ION 1	FOR	SEQ :	ID N	0: 1	:			•		•
50				. 1					٠				*:	
51		(i)				ARAC'								
52			•	-		: 60		-	irs					
53			•	•		nucl								
54				-		EDNE		_	le		•			
55			(D) TOI	POLO	GY:	line	ar						
56														
57		(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: SI	EQ I	D NO	: 1:			
8														
59	CTC	CTGCA	GT T	GGAC	CTGT	G CC	ATGG	CCGG	CTG	GGCC	GCA ?	l'AGA	ATGG	AA
50	CAA	CTAAA	3C											
51														
52	(2)	INFO	RMAT	ION 1	FOR :	SEQ :	ID N	0: 2	:					
53			-						•					
54		(i)	SEQ	UENC	E CH	ARAC'	reri:	STIC	S:					
55			(A) LEI	NGTH	: 92	ami	no a	cids					
56			(B) TYI	PE: a	amin	o ac	id ,						
57			(C) STI	RAND	EDNE	SS:							
8			(D) TO	POLO	GY: 1	unkne	own						
59														
70		(ii)	MOLI	ECULI	E TY	PE:]	prot	ein					•	
71														
72														
73		(xi)	SEQ	JENCI	E DE	SCRI	PTIO	N: S1	EQ I	D NO	: 2:			
74														
75		Met	Ala	Glu	Glu	Arg	Pro	Tyr	Ala	Cys	Pro			
76						5					10			
77														
78		Val	Glu	Ser	Cys	Asp	Arg	Arg	Phe	Ser	Arg			
79						15					20			
30														
31		Ser	Asp	Glu	Leu	Thr	Arg	His	Ile	Arg	Ile			
32						25					30			
33														
34		His	Thr	Gly	Gln	Lys	Pro	Phe	Gln	Cys	Arg			
35						35					40			
36														
37		Ile	Cys	Met	Arg	Asn	Phe	Ser	Xaa	Xaa	Xaa			
88						45					50			
39														
90		Xaa	Leu	Xaa	Xaa	His	Xaa	Arg	Thr	His	Thr			
91						55					60			
92														
93	Þ	Gly	Glu	Lys	Pro	Phe	Ala	Cys	Asp	Ile	Cys			
1						65		-	_		70			
95														
96		Gly	Arg	Lys	Phe	Ala	Arg	Ser	Asp	Glu	Arg			
7						75			_		80			
8	•													
9		Lys	Arg	His	Thr	Lys	Ile	His	Leu	Arg	Gln			

149 150

151 152 GCGTATATAC GCCCACGCTA TATA

(2) INFORMATION FOR SEQ ID NO: 7:

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24

INPUT SET: S20569.raw 100 85 90 101 102 Lys Asp 103 104 (2) INFORMATION FOR SEQ ID NO: 3: 105 106 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs 107 108 (B) TYPE: nucleic acid 109 (C) STRANDEDNESS: single 110 (D) TOPOLOGY: linear 111 112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: 113 TATGACTTGG ATGGGAGACC GCCTGG 114 26 115 116 (2) INFORMATION FOR SEQ ID NO: 4: 117 (i) SEQUENCE CHARACTERISTICS: 118 119 (A) LENGTH: 28 base pairs 120 (B) TYPE: nucleic acid (C) STRANDEDNESS: single 121 122 (D) TOPOLOGY: linear 123 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: 124 125 126 AATTCCAGGC GGTCTCCCAT CCAAGTCA 28 127 128 (2) INFORMATION FOR SEQ ID NO: 5: 129 130 (i) SEQUENCE CHARACTERISTICS: 131 (A) LENGTH: 21 base pairs 132 (B) TYPE: nucleic acid 133 (C) STRANDEDNESS: single 134 (D) TOPOLOGY: linear 135 136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: 137 138 TATATAGCGT GGGCGTATAT A 21 139 140 (2) INFORMATION FOR SEQ ID NO: 6: 141 142 (i) SEQUENCE CHARACTERISTICS: 143 (A) LENGTH: 24 base pairs 144 (B) TYPE: nucleic acid 145 (C) STRANDEDNESS: single 146 (D) TOPOLOGY: linear 147 148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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:		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 21 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(b) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
TATA	ATAGCGN NNGCGTATAT A	21
(2)	INFORMATION FOR SEQ ID NO: 8:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 24 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
	· · -	
GCGI	TATATAC GCNNNCGCTA TATA	24
(2)	INFORMATION FOR SEQ ID NO: 9:	+
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 33 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
TTCC	CATGGAG ACGCAGAAGC CCTTCAGCGG CCA	33
121	THEODMATION FOR SEC ID NO. 10.	
(~)	INFORMATION FOR SEQ ID NO: 10:	
	(i) SEQUENCE CHARACTERISTICS:	
	• • • • • • • • • • • • • • • • • • • •	
	(A) LENGTH: 33 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
	(vr) pedopuce percutition: sed in uo: in:	
ጥጥረር	CATGGAG ACGCAGGTGA GTTCCTGACG CCA	33
1100	CATCORD ACCORDING GITCCIONCO CON	33
(2)	INFORMATION FOR SEO EID NO: 11:	
(4)	THE OTHER POR DESIGNATION TO. II.	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 33 base pairs	
	(A) DENGIN: 35 Dase pairs	

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•	The state of the s
206	(C) STRANDEDNESS: single
207	(D) TOPOLOGY: linear
208	(3) 101020011 1211001
209	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
210	(MI) DEPOSITED DESCRIPTION. DEP ID NO. 11.
211	CCCCTTTCTC TTCCAGAAGC CCTTCAGCGG CCA
212	CCCCTTTCTC TTCCAGAAGC CCTTCAGCGG CCA
213	(2) INFORMATION FOR SEQ ID NO: 12:
214	(2) INFORMATION FOR DEQ ID NO. 12.
215	(i) SEQUENCE CHARACTERISTICS:
216	(A) LENGTH: 33 amino acids
217	(B) TYPE: amino acid
218	(C) STRANDEDNESS:
219	(D) TOPOLOGY: unknown
220	(b) for older: diknown
221	(ii) MOLECULE TYPE: peptide
222	(11) Monneoun 11FE. peptide
223	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
224	(AI) DECORACE DESCRIPTION. DEC 1D NO. 12.
225	Met Ala Glu Glu Lys Pro Phe Gln Cys Arg
226	5 10
227	
228	Ile Cys Met Arg Asn Phe Ser Asp Arg Ser
229	15 20
230	13 20
231	Ser Leu Thr Arg His Thr Arg His Thr Gly
232	25 30
233	
234	Glu Lys Pro
235	322 273 744
236	(2) INFORMATION FOR SEQ ID NO: 13:
237	(-,
238	(i) SEQUENCE CHARACTERISTICS:
239	(A) LENGTH: 33 amino acids
240	(B) TYPE: amino acid
241	(C) STRANDEDNESS:
242	(D) TOPOLOGY: unknown
243	
244	(ii) MOLECULE TYPE: peptide
245	• •
246	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
247	
248	Met Ala Glu Glu Lys Pro Phe Gln Cys Arg
249	5 10
250	
251	Ile Cys Met Arg Asn Phe Ser Glu Arg Gly
252	15 20
253	
254	Thr Leu Ala Arg His Glu Lys His Thr Gly
255	25 30
256	
257	Glu Lys Pro
258	
	•



SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/793,408

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